

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BRASH, ALAN R.
BOEGLIN, WILLIAM E.
JISAKA, MITSUO

(ii) TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND
NUCLEIC ACIDS

(iii) NUMBER OF SEQUENCES: 36

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ARLES A. TAYLOR, JR.

(B) STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER
BOULEVARD

(C) CITY: DURHAM

(D) STATE: NORTH CAROLINA

(E) COUNTRY: USA

(F) ZIP: 27707

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

(B) COMPUTER: IBM PC/XT/AT compatible

(C) OPERATING SYSTEM: Windows 3.1

(D) SOFTWARE: WORD PERFECT 6.1 and ASCII

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/061,768

(B) FILING DATE: April 16, 1998

(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA: None

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: ARLES A. TAYLOR, JR.

(B) REGISTRATION NUMBER: 39,395

(C) REFERENCE/DOCKET NUMBER: 1242/5

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (919) 493-8000

(B) TELEFAX: (919) 419-0383

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2685 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGGCGTGTC CCAGGGGGAG CCCCCTCTG CAGCCCTGTG CGCCGTAGAG AGCTGGACTT 60

5 AGGCTGGCAG C ATG GCC GAG TTC AGG GTC AGG GTG TCC ACC GGA GAA GCC 110

Met Ala Glu Phe Arg Val Arg Val Ser Thr Gly Glu Ala

1 5 10

TTC GGG GCT GGC ACA TGG GAC AAA GTG TCT GTC AGC ATC GTG GGG ACC 158

10 Phe Gly Ala Gly Thr Trp Asp Lys Val Ser Val Ser Ile Val Gly Thr

15 20 25

CGG GGA GAG AGC CCC CCA CTG CCC CTG GAC AAT CTC GGC AAG GAG TTC 206

Arg Gly Glu Ser Pro Pro Leu Pro Leu Asp Asn Leu Gly Lys Glu Phe

15 30 35 40 45

ACT GCG GGC GCT GAG GAG GAC TTC CAG GTG ACG CTC CCG GAG GAC GTA 254

Thr Ala Gly Ala Glu Glu Asp Phe Gln Val Thr Leu Pro Glu Asp Val

50 55 60

20 GGC CGA GTG CTG CTG CTG CGC GTG CAC AAG GCG CCC CCA GTG CTG CCC 302

Gly Arg Val Leu Leu Leu Arg Val His Lys Ala Pro Pro Val Leu Pro

65 70 75

25 CTG CTG GGG CCC CTG GCC CCG GAT GCC TGG TTC TGC CGC TGG TTC CAG 350

Leu Leu Gly Pro Leu Ala Pro Asp Ala Trp Phe Cys Arg Trp Phe Gln

80 85 90

CTG ACA CCG CCG CGG GGC GGC CAC CTC CTC TTC CCC TGC TAC CAG TGG 398

30 Leu Thr Pro Pro Arg Gly Gly His Leu Leu Phe Pro Cys Tyr Gln Trp

95 100 105

CTG GAG GGG GCG GGG ACC CTG GTG CTG CAG GAG GGT ACA GCC AAG GTG 446

Leu Glu Gly Ala Gly Thr Leu Val Leu Gln Glu Gly Thr Ala Lys Val

35 110 115 120 125

TCC TGG GCA GAC CAC CAC CCT GTG CTC CAG CAA CAG CGC CAG GAG GAG 494

Ser Trp Ala Asp His His Pro Val Leu Gln Gln Gln Arg Gln Glu Glu

130 135 140

	CTT CAG GCC CGG CAG GAG ATG TAC CAG TGG AAG GCT TAC AAC CCA GGT	542
	Leu Gln Ala Arg Gln Glu Met Tyr Gln Trp Lys Ala Tyr Asn Pro Gly	
	145 150 155	
5	TGG CCT CAC TGC CTG GAT GAA AAG ACA GTG GAA GAC TTG GAG CTC AAT	590
	Trp Pro His Cys Leu Asp Glu Lys Thr Val Glu Asp Leu Glu Leu Asn	
	160 165 170	
10	ATC AAA TAC TCC ACA GCC AAG AAT GCC AAC TTT TAT CTA CAA GCT GGC	638
	Ile Lys Tyr Ser Thr Ala Lys Asn Ala Asn Phe Tyr Leu Gln Ala Gly	
	175 180 185	
	TCT GCT TTT GCA GAG ATG AAA ATC AAG GGG TTG CTG GAC CGC AAG GGG	686
15	Ser Ala Phe Ala Glu Met Lys Ile Lys Gly Leu Leu Asp Arg Lys Gly	
	190 195 200 205	
	CTC TGG AGG AGT CTG AAT GAG ATG AAA AGG ATC TTC AAC TTC CGG AGG	734
	Leu Trp Arg Ser Leu Asn Glu Met Lys Arg Ile Phe Asn Phe Arg Arg	
20	210 215 220	
	ACC CCA GCA GCT GAG CAC GCA TTT GAG CAC TGG CAG GAG GAT GCC TTC	782
	Thr Pro Ala Ala Glu His Ala Phe Glu His Trp Gln Glu Asp Ala Phe	
	225 230 235	
25	TTC GCC TCC CAG TTC CTG AAT GGT CTC AAC CCT GTC CTG ATC CGC CGC	830
	Phe Ala Ser Gln Phe Leu Asn Gly Leu Asn Pro Val Leu Ile Arg Arg	
	240 245 250	
30	TGT CAC TAC CTC CCA AAG AAC TTC CCC GTC ACT GAT GCC ATG GTG GCC	878
	Cys His Tyr Leu Pro Lys Asn Phe Pro Val Thr Asp Ala Met Val Ala	
	255 260 265	
	TCA TTG TTG GGT CCT GGG ACC AGC TTG CAG GCT GAG CTA GAG AAG GGC	926
35	Ser Leu Leu Gly Pro Gly Thr Ser Leu Gln Ala Glu Leu Glu Lys Gly	
	270 275 280 285	
	TCC CTG TTC TTG GTG GAT CAC GGC ATC CTC TCT GGC ATC CAG ACC AAT	974
	Ser Leu Phe Leu Val Asp His Gly Ile Leu Ser Gly Ile Gln Thr Asn	
40	290 295 300	

GTC ATT AAT GGG AAG CCG CAG TTC TCT GCG GCC CCA ATG ACC CTG CTA 1022

Val Ile Asn Gly Lys Pro Gln Phe Ser Ala Ala Pro Met Thr Leu Leu

305

310

315

5

TAC CAG AGC CCA GGC TGC GGG CCG CTG CTG CCT CTC GCC ATC CAG CTC 1070

Tyr Gln Ser Pro Gly Cys Gly Pro Leu Leu Pro Leu Ala Ile Gln Leu

320

325

330

10

AGC CAG ACC CCC GGC CCA AAC AGC CCC ATC TTC CTG CCC ACT GAT GAC 1118

Ser Gln Thr Pro Gly Pro Asn Ser Pro Ile Phe Leu Pro Thr Asp Asp

335

340

345

AAG TGG GAC TGG TTG CTG GCC AAG ACC TGG GTG CGC AAT GCC GAG TTC 1166

Lys Trp Asp Trp Leu Leu Ala Lys Thr Trp Val Arg Asn Ala Glu Phe

15

350

355

360

365

TCC TTC CAT GAG GCC CTC ACG CAC CTG CTG CAC TCA CAT CTG CTG CCT 1214

Ser Phe His Glu Ala Leu Thr His Leu Leu His Ser His Leu Leu Pro

370

375

380

20

GAG GTC TTC ACC CTG GCT ACC CTG CGT CAG CTG CCC CAC TGC CAC CCT 1262

Glu Val Phe Thr Leu Ala Thr Leu Arg Gln Leu Pro His Cys His Pro

385

390

395

25

CTC TTC AAG CTG CTG ATC CCG CAC ACC CGA TAC ACC CTG CAC ATC AAC 1310

Leu Phe Lys Leu Leu Ile Pro His Thr Arg Tyr Thr Leu His Ile Asn

400

405

410

30

ACA CTC GCC CGG GAG CTG CTT ATC GTG CCA GGG CAG GTG GTG GAC AGG 1358

Thr Leu Ala Arg Glu Leu Leu Ile Val Pro Gly Gln Val Val Asp Arg

415

420

425

35

TCC ACA GGC ATC GGC ATT GAA GGC TTC TCT GAG TTG ATA CAG AGG AAC 1406

Ser Thr Gly Ile Gly Ile Glu Gly Phe Ser Glu Leu Ile Gln Arg Asn

430

435

440

445

ATG AAG CAG CTG AAC TAT TCT CTC CTG TGT CTG CCT GAG GAT ATC CGG 1454

Met Lys Gln Leu Asn Tyr Ser Leu Leu Cys Leu Pro Glu Asp Ile Arg

450

455

460

40

ACC CGA GGA GTT GAA GAC ATC CCA GGC TAC TAC TAC CGT GAT GAT GGG 1502

Thr Arg Gly Val Glu Asp Ile Pro Gly Tyr Tyr Tyr Arg Asp Asp Gly

465

470

475

5

ATG CAG ATT TGG GGT GCA GTG GAA CGC TTT GTC TCT GAA ATC ATC GGT 1550

Met Gln Ile Trp Gly Ala Val Glu Arg Phe Val Ser Glu Ile Ile Gly

480

485

490

ATC TAC TAC CCA AGT GAT GAG TCT GTC CAA GAT GAC AGA GAG CTC CAG 1598

Ile Tyr Tyr Pro Ser Asp Glu Ser Val Gln Asp Asp Arg Glu Leu Gln

495

500

505

10

GCC TGG GTC AGA GAG ATC TTC TCC AAG GGC TTC CTA AAC CAG GAG AGC 1646

Ala Trp Val Arg Glu Ile Phe Ser Lys Gly Phe Leu Asn Gln Glu Ser

510

515

520

525

15

TCA GGT ATC CCT TCC TCA CTG GAG ACC CGG GAA GCC CTG GTG CAG TAT 1694

Ser Gly Ile Pro Ser Ser Leu Glu Thr Arg Glu Ala Leu Val Gln Tyr

530

535

540

20

GTC ACC ATG GTG ATA TTC ACC TGC TCA GCC AAG CAT GCG GCT GTC AGT 1742

Val Thr Met Val Ile Phe Thr Cys Ser Ala Lys His Ala Ala Val Ser

545

550

555

25

GCA GGG CAG TTT GAC TCC TGT GCT TGG ATG CCC AAC CTG CCA CCC AGC 1790

Ala Gly Gln Phe Asp Ser Cys Ala Trp Met Pro Asn Leu Pro Pro Ser

560

565

570

ATG CAG CTG CCA CCA CCC ACC TCC AAA GGC CTG GCA ACA TGC GAG GGC 1838

Met Gln Leu Pro Pro Pro Thr Ser Lys Gly Leu Ala Thr Cys Glu Gly

575

580

585

30

TTC ATA GCC ACC CTC CCA CCT GTC AAT GCC ACA TGT GAT GTC ATC CTT 1886

Phe Ile Ala Thr Leu Pro Pro Val Asn Ala Thr Cys Asp Val Ile Leu

590

595

600

605

35

GCT CTC TGG TTG CTG AGC AAG GAG CCT GGA GAC CAA AGG CCC CTG GGC 1934

Ala Leu Trp Leu Leu Ser Lys Glu Pro Gly Asp Gln Arg Pro Leu Gly

610

615

620

40

ACC TAT CCG GAT GAG GAG TTC ACA GAG GAG GCC CCT CGG CGG AGC ATC 2032
 Thr Tyr Pro Asp Glu His Phe Thr Glu Glu Ala Pro Arg Arg Ser Ile
 625 630 635

5 GCC ACC TTC CAG AGC CGC CTG GCC CAG ATC TCG AGG GGC ATC CAG GAG 2030
 Ala Thr Phe Gln Ser Arg Leu Ala Gln Ile Ser Arg Gly Ile Gln Glu
 640 645 650

10 CGG AAC CGG GGC CTG GTG CTG CCC TAC ACC TAC CTA GAC CCT CCC CTC 2078
 Arg Asn Arg Gly Leu Val Leu Pro Tyr Thr Tyr Leu Asp Pro Pro Leu
 655 660 665

15 ATC GAG AAC AGC GTC TCC ATC TAAATCCCAG GGGAACACAG GCCCAGATGA 2129
 Ile Glu Asn Ser Val Ser Ile
 670 675

CATCCCTTTG ACCACATCGC TCTAGGATAA CTGGCACCCA GAGAAAAGGA CTCCTCAGAA 2189

20 AAAACAGGCC CCCATGTGCC TCTCCTGGGA CAACCAGACT CTGTAACTCA CCCCACCAC 2249

CATACACACA CACAAAAACA GAAACAAAAT CAAAACAGAG AAAGCAGAAA ATCTACCAAG 2309

AACAGAGTCT CAGGACAGAA CCACTGAGTC TTTTGGAGGC TCCAAGCCTC AAAGTGCCCG 2369

25 CAGAGCCCAC CTTGAGGGTT TTGCTAGTTG GTTTTGT TTTT GCGTTTACAG CCGTGGGGGG 2429

AAGCACATAA TCCCGCCCCA GGGCCCACTA GCATCCACTG ATTGGACCTT ATGGTCACCC 2489

30 AACTCAAGGA CAGCCACCAA GAAGTGGCTG CCAAAGAGAC TGGGCGCAGT GGCTCATGCC 2549

CATAATCCCA GCACTTTGGG AGATGGAGGC GGGAAAATCA TTTGAGGTCA GAAGTTCAAG 2609

GCCAGCCTGG ACGACATAGC GAGACTCCAC CTCTACCAAA AAATAAAAAT TAAAAACAA 2669

35 AAAAAAAAAA AAAAAA 2685

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 676 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Ala	Glu	Phe	Arg	Val	Arg	Val	Ser	Thr	Gly	Glu	Ala	Phe	Gly	Ala
	1				5						10					15
5	Gly	Thr	Trp	Asp	Lys	Val	Ser	Val	Ser	Ile	Val	Gly	Thr	Arg	Gly	Glu
					20					25						30
	Ser	Pro	Pro	Leu	Pro	Leu	Asp	Asn	Leu	Gly	Lys	Glu	Phe	Thr	Ala	Gly
					35					40						45
10	Ala	Glu	Glu	Asp	Phe	Gln	Val	Thr	Leu	Pro	Glu	Asp	Val	Gly	Arg	Val
					50					55						60
	Leu	Leu	Leu	Arg	Val	His	Lys	Ala	Pro	Pro	Val	Leu	Pro	Leu	Leu	Gly
15					65					70						75
																80
	Pro	Leu	Ala	Pro	Asp	Ala	Trp	Phe	Cys	Arg	Trp	Phe	Gln	Leu	Thr	Pro
										85						95
20	Pro	Arg	Gly	Gly	His	Leu	Leu	Phe	Pro	Cys	Tyr	Gln	Trp	Leu	Glu	Gly
					100					105						110
	Ala	Gly	Thr	Leu	Val	Leu	Gln	Glu	Gly	Thr	Ala	Lys	Val	Ser	Trp	Ala
					115					120						125
25	Asp	His	His	Pro	Val	Leu	Gln	Gln	Gln	Arg	Gln	Glu	Glu	Leu	Gln	Ala
					130					135						140
	Arg	Gln	Glu	Met	Tyr	Gln	Trp	Lys	Ala	Tyr	Asn	Pro	Gly	Trp	Pro	His
30					145					150						155
																160
	Cys	Leu	Asp	Glu	Lys	Thr	Val	Glu	Asp	Leu	Glu	Leu	Asn	Ile	Lys	Tyr
					165					170						175
35	Ser	Thr	Ala	Lys	Asn	Ala	Asn	Phe	Tyr	Leu	Gln	Ala	Gly	Ser	Ala	Phe
					180					185						190
	Ala	Glu	Met	Lys	Ile	Lys	Gly	Leu	Leu	Asp	Arg	Lys	Gly	Leu	Trp	Arg
					195					200						205
40	Ser	Leu	Asn	Glu	Met	Lys	Arg	Ile	Phe	Asn	Phe	Arg	Arg	Thr	Pro	Ala
					210					215						220

Ala Glu His Ala Phe Glu His Trp Gln Glu Asp Ala Phe Phe Ala Ser
 225 230 235 240

5 Gln Phe Leu Asn Gly Leu Asn Pro Val Leu Ile Arg Arg Cys His Tyr
 245 250 255

Leu Pro Lys Asn Phe Pro Val Thr Asp Ala Met Val Ala Ser Leu Leu
 260 265 270

10 Gly Pro Gly Thr Ser Leu Gln Ala Glu Leu Glu Lys Gly Ser Leu Phe
 275 280 285

Leu Val Asp His Gly Ile Leu Ser Gly Ile Gln Thr Asn Val Ile Asn
 290 295 300

15 Gly Lys Pro Gln Phe Ser Ala Ala Pro Met Thr Leu Leu Tyr Gln Ser
 305 310 315 320

Pro Gly Cys Gly Pro Leu Leu Pro Leu Ala Ile Gln Leu Ser Gln Thr
 20 325 330 335

Pro Gly Pro Asn Ser Pro Ile Phe Leu Pro Thr Asp Asp Lys Trp Asp
 340 345 350

25 Trp Leu Leu Ala Lys Thr Trp Val Arg Asn Ala Glu Phe Ser Phe His
 355 360 365

Glu Ala Leu Thr His Leu Leu His Ser His Leu Leu Pro Glu Val Phe
 370 375 380

30 Thr Leu Ala Thr Leu Arg Gln Leu Pro His Cys His Pro Leu Phe Lys
 385 390 395 400

Leu Leu Ile Pro His Thr Arg Tyr Thr Leu His Ile Asn Thr Leu Ala
 35 405 410 415

Arg Glu Leu Leu Ile Val Pro Gly Gln Val Val Asp Arg Ser Thr Gly
 420 425 430

40 Ile Gly Ile Glu Gly Phe Ser Glu Leu Ile Gln Arg Asn Met Lys Gln
 435 440 445

Leu Asn Tyr Ser Leu Leu Cys Leu Pro Glu Asp Ile Arg Thr Arg Gly
 450 455 460

Val Glu Asp Ile Pro Gly Tyr Tyr Tyr Arg Asp Asp Gly Met Gln Ile

465 470 475 480

5 Trp Gly Ala Val Glu Arg Phe Val Ser Glu Ile Ile Gly Ile Tyr Tyr

485 490 495

Pro Ser Asp Glu Ser Val Gln Asp Asp Arg Glu Leu Gln Ala Trp Val

500

10 Arg Glu Ile Phe Ser Lys Gly Phe Leu Asn Gln Glu Ser Ser Gly Ile

515

Pro Ser Ser Leu Glu Thr Arg Glu Ala Leu Val Gln Tyr Val Thr Met

15 530 535 540

Val Ile Phe Thr Cys Ser Ala Lys His Ala Ala Val Ser Ala Gly Gln

545 550 555 560

20 Phe Asp Ser Cys Ala Trp Met Pro Asn Leu Pro Pro Ser Met Gln Leu

565

Pro Pro Pro Thr Ser Lys Gly Leu Ala Thr Cys Glu Gly Phe Ile Ala

580

25 Thr Leu Pro Pro Val Asn Ala Thr Cys Asp Val Ile Leu Ala Leu Trp

595

Leu Leu Ser Lys Glu Pro Gly Asp Gln Arg Pro Leu Gly Thr Tyr Pro

30 610 615 620

Asp Glu His Phe Thr Glu Glu Ala Pro Arg Arg Ser Ile Ala Thr Phe

625 630 635 640

Gln Ser Arg Leu Ala Gln Ile Ser Arg Gly Ile Gln Glu Arg Asn Arg

35

Gly Leu Val Leu Pro Tyr Thr Tyr Leu Asp Pro Pro Leu Ile Glu Asn

660

40 Ser Val Ser Ile

675

- (2) INFORMATION FOR SEQ ID NO:3:
 (i). SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	ATG GCG AAA TGC AGG GTG AGA GTA TCC ACG GGG GAA GCC TGT GGG GCT	48
10	Met Ala Lys Cys Arg Val Arg Val Ser Thr Gly Glu Ala Cys Gly Ala	
	1 5 10 15	
	GGC ACA TGG GAC AAA GTG TCT GTC AGC ATC GTG GGA ACC CAC GGA GAG	96
	Gly Thr Trp Asp Lys Val Ser Val Ser Ile Val Gly Thr His Gly Glu	
15	20 25 30	
	AGC CCC TTA GTA CCT CTG GAC CAT CTG GGC AAG GAG TTC AGC GCC GGT	144
	Ser Pro Leu Val Pro Leu Asp His Leu Gly Lys Glu Phe Ser Ala Gly	
	35 40 45	
20	GCT GAA GAA GAC TTC GAG GTG ACG CTT CCC CAG GAC GTA GGC ACT GTG	192
	Ala Glu Glu Asp Phe Glu Val Thr Leu Pro Gln Asp Val Gly Thr Val	
	50 55 60	
25	CTG ATG CTG CGA GTC CAC AAA GCA CCC CCG GAA GTG TCC CTC CCG CTT	240
	Leu Met Leu Arg Val His Lys Ala Pro Pro Glu Val Ser Leu Pro Leu	
	65 70 75 80	
	ATG TCT TTC CGT TCT GAT GCC TGG TTC TGC CGC TGG TTC GAG CTG GAG	288
	Met Ser Phe Arg Ser Asp Ala Trp Phe Cys Arg Trp Phe Glu Leu Glu	
30	85 90 95	
	TGG CTA CCT GGG GCT GCA CTC CAC TTC CCC TGT TAT CAG TGG CTG GAA	336
	Trp Leu Pro Gly Ala Ala Leu His Phe Pro Cys Tyr Gln Trp Leu Glu	
	100 105 110	
	GGG GCG GGG GAG CTG GTG CTG AGA GAG GGA GCA GCA AAG GTG TCC TGG	384
35	Gly Ala Gly Glu Leu Val Leu Arg Glu Gly Ala Ala Lys Val Ser Trp	
	115 120 125	
	CAA GAC CAT CAC CCT ACA CTG CAG GAT CAG CGC CAG AAG GAG CTT GAG	432
	Gln Asp His His Pro Thr Leu Gln Asp Gln Arg Gln Lys Glu Leu Glu	
40	130 135 140	

TCC AGG CAG AAG ATG TAC AGC TGG AAG ACT TAC ATT GAA GGT TGG CCT 480
 Ser Arg Gln Lys Met Tyr Ser Trp Lys Thr Tyr Ile Glu Gly Trp Pro
 145 150 155 160
 5
 CGC TGC CTT GAC CAC GAG ACT GTG AAA GAC TTG GAC CTC AAC ATC AAG 528
 Arg Cys Leu Asp His Glu Thr Val Lys Asp Leu Asp Leu Asn Ile Lys
 165 170 175
 TAC TCT GCG ATG AAG AAT GCC AAA CTC TTC TTT AAA GCC CAC TCC GCG 576
 Tyr Ser Ala Met Lys Asn Ala Lys Leu Phe Phe Lys Ala His Ser Ala
 180 185 190
 10
 TAT ACG GAG CTG AAA GTC AAA GGG CTC CTG GAC CGC ACA GGA CTC TGG 624
 Tyr Thr Glu Leu Lys Val Lys Gly Leu Leu Asp Arg Thr Gly Leu Trp
 195 200 205
 15
 AGG AGT CTG AGG GAG ATG AGA AGG CTG TTT AAC TTC CGC AAG ACT CCA 672
 Arg Ser Leu Arg Glu Met Arg Arg Leu Phe Asn Phe Arg Lys Thr Pro
 210 215 220
 20
 GCA GCA GAG TAT GTG TTT GCA CAC TGG CAG GAA GAT GCC TTC TTC GCC 720
 Ala Ala Glu Tyr Val Phe Ala His Trp Gln Glu Asp Ala Phe Phe Ala
 225 230 235 240
 TCC CAG TTC CTA AAT GGC ATC AAC CCG GTC CTG ATT CGC CGC TGT CAC 768
 Ser Gln Phe Leu Asn Gly Ile Asn Pro Val Leu Ile Arg Arg Cys His
 245 250 255
 AGT CTC CCA AAC AAC TTC CCG GTC ACT GAT GAA ATG GTG GCC CCA GTG 816
 Ser Leu Pro Asn Asn Phe Pro Val Thr Asp Glu Met Val Ala Pro Val
 260 265 270
 30
 CTG GGC CCT GGA ACC AGT CTG CAG GCT GAG TTG GAG AAG GGC TCC CTG 864
 Leu Gly Pro Gly Thr Ser Leu Gln Ala Glu Leu Glu Lys Gly Ser Leu
 275 280 285
 35
 TTC TTG GTG GAT CAT GGC ATT CTT TCT GGA GTC CAC ACC AAC ATC CTC 912
 Phe Leu Val Asp His Gly Ile Leu Ser Gly Val His Thr Asn Ile Leu
 290 295 300
 40

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CAG CTG AAC TAC TCT GTC CTG TGT CTC CCT GAA GAT ATC CGA GCC CGA 1392
 Gln Leu Asn Tyr Ser Val Leu Cys Leu Pro Glu Asp Ile Arg Ala Arg
 450 455 460

GGT GTG GAA GAC ATC GGC TAC TAT TAC CGA GAT GAT GGG ATG CAG
Gly Val Glu Asp Ile Pro Gly Tyr Tyr Tyr Arg Asp Asp Gly Met Gln
465 470 475 480

5 ATC TGG GGG GCA ATA AAG AGC TTT GTC TCT GAA ATA GTC AGC ATC TAC 1488
Ile Trp Gly Ala Ile Lys Ser Phe Val Ser Glu Ile Val Ser Ile Tyr
485 490 495

10 TAT CCA AGT GAC ACA TCC GTC CAA GAT GAC CAA GAG CTC CAG GCC TGG 1536
Tyr Pro Ser Asp Thr Ser Val Gln Asp Asp Gln Glu Leu Gln Ala Trp
500 505 510

15 GTG AGG GAG ATC TTC TCT GAG GGC TTC CTC GGC CGA GAA AGC TCA GGT 1584
Val Arg Glu Ile Phe Ser Glu Gly Phe Leu Gly Arg Glu Ser Ser Gly
515 520 525

ATG CCC TCC TTG TTG GAT ACC CGG GAA GCC CTG GTC CAG TAT ATC ACC 1632
Met Pro Ser Leu Leu Asp Thr Arg Glu Ala Leu Val Gln Tyr Ile Thr
530 535 540

20 ATG GTG ATA TTC ACC TGC TCA GCC AAG CAT GCA GCT GTC AGT TCA GGC 1680
Met Val Ile Phe Thr Cys Ser Ala Lys His Ala Ala Val Ser Ser Gly
545 550 555 560

25 CAG TTC GAC TCT TGT GTT TGG ATG CCC AAT CTG CCA CCT ACC ATG CAG 1728
Gln Phe Asp Ser Cys Val Trp Met Pro Asn Leu Pro Pro Thr Met Gln
565 570 575

30 CTA CCA CCA CCT ACT TCC AAA GGC CAG GCC CGG CCT GAG AGT TTC ATA 1776
Leu Pro Pro Pro Thr Ser Lys Gly Gln Ala Arg Pro Glu Ser Phe Ile
580 585 590

35 GCC ACG CTC CCA GCA GTT AAT TCG TCA AGT TAT CAC ATC ATT GCT CTC 1824
Ala Thr Leu Pro Ala Val Asn Ser Ser Ser Tyr His Ile Ile Ala Leu
595 600 605

40 TGG CTG CTA AGC GCA GAA CCT GGG GAC CAA AGG CCC CTG GGC CAC TAT 1872
Trp Leu Leu Ser Ala Glu Pro Gly Asp Gln Arg Pro Leu Gly His Tyr
610 615 620

CCA GAT GAA CAC TTC AAG GAG GAT GCC CCC CGG CGA AGC GTG GCT GCC 1968
Pro Asp Glu His Phe Thr Glu Asp Ala Pro Arg Arg Ser Val Ala Ala
625 630 635 640

5 TTC CAG AGA AAG CTG ATC CAG ATC TCC AAG GGC ATC AGG GAG AGG AAC 1968
Phe Gln Arg Lys Leu Ile Gln Ile Ser Lys Gly Ile Arg Glu Arg Asn
645 650 655

10 CGA GGC CTG GCA CTG CCC TAC ACC TAC CTG GAT CCT CCC CTC ATT GAG 2016
Arg Gly Leu Ala Leu Pro Tyr Thr Tyr Leu Asp Pro Pro Leu Ile Glu
660 665 670

15 AAC AGT GTC TCC ATC TAACATCTTG GAGAAGACAG TCCTGTGTGA CATATAGAAC 2071
Asn Ser Val Ser Ile
675

TCTTGACCAT GCCTCTCCAG GCTAAGTCCC CGTATGCTTC TCCTGGACAA CCAAGCCCCA 2131

20 TCTTACACAC ACACACACAC ACACACACCT AATAAAATCG AAACAGAAAA ACCTAAACTC 2191

CCACAGAAGG CAAGATCTCA CACAGCAGAG AGCCATCCAA ATGTTTGGAG ACCCTGAGCT 2251

TCAGCTCTGA TTAACGGCTT TGCTGGTTTG CTTTGCTTTC TATTCCATTA ACCATGGACG 2311

25 GTAACAGAAA GCACAGAACC CTGGTTCACCT GCACAAAGCC ACTGAGATCT CACCCTCACC 2371

TGACACAAAG GCAGCTATCA TACAGGCTTA TCAGGAACAC AGGAATTTGT CCAATCAAAG 2431

30 CCTACCCACT AGGTCCATCG TGACCTACGA CCTCACACTG GCATGCTTTA GCTTTGAGAA 2491

GGGATTACTG GAGTCAGGTA CGAAGAGAAG GACAGGACGA AGGCATGGCT CCATGTGGAA 2551

GAACATATCT GCTCTTCCAG ATGACCAGGG TAGCTCACAG CCATGTGTCA TTCTAACTCC 2611

35 AGAGGTCTCT AGTGGCCATG AAGACTCCAG GCATTCAGGG GATATACCAG TAGACACCAA 2671

AATTATACTT TTTAAGAGAG AGGATGGGCT GGAGAGATGG CTCAGCGGTT AAGAGCACTG 2731

ACTGCTCTTC CAGAGATCCT GAGTTCAATT CCCAGCAACC ACATGGTGGC TCACAACCAT 2791

40 CTGTAATGGG ATTCGATGCC CTCTTCTGGC GTGTCTGAAG ACAGCGACAG TGTATGCACA 2851

TATATAAAAT AAATAAATCT TAAAAAACA AAACAAGAGA GAGGGACATG CTACCATTTC 2911

45 TACCTCACTT CTCTCAAAG CCACCCCTAA AGTGAATTGT GAACCAGGTC CCCTTTGCAG 2971

AGAGTTAGAA GATATTCTCA AACCTCTAAT ACCTTCACAT CTAAATCCA TCTTCATTCC 3031
 AAAATTCCAA TATTTTATAT ACACTCTCCA GTTTGGTGGG TGAGGGGTG TTTTGTGTT 3091
 5 GGTGTTGGTT GGTGGGGTT TTGTTTTGT TTTGATTTT GTTTTCTCT GGTTCAGACT 3151
 CCATGGACGT TCATTAATGT CATAAATGAG TTCATTCCAA AAAAAAAAAA AAAA 3205

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- 15 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Met	Ala	Lys	Cys	Arg	Val	Arg	Val	Ser	Thr	Gly	Glu	Ala	Cys	Gly	Ala	
	1					5					10					15	
20	Gly	Thr	Trp	Asp	Lys	Val	Ser	Val	Ser	Ile	Val	Gly	Thr	His	Gly	Glu	
						20					25					30	
	Ser	Pro	Leu	Val	Pro	Leu	Asp	His	Leu	Gly	Lys	Glu	Phe	Ser	Ala	Gly	
						35					40					45	
25	Ala	Glu	Glu	Asp	Phe	Glu	Val	Thr	Leu	Pro	Gln	Asp	Val	Gly	Thr	Val	
						50					55					60	
	Leu	Met	Leu	Arg	Val	His	Lys	Ala	Pro	Pro	Glu	Val	Ser	Leu	Pro	Leu	
30						65					70					80	
	Met	Ser	Phe	Arg	Ser	Asp	Ala	Trp	Phe	Cys	Arg	Trp	Phe	Glu	Leu	Glu	
						85					90					95	
35	Trp	Leu	Pro	Gly	Ala	Ala	Leu	His	Phe	Pro	Cys	Tyr	Gln	Trp	Leu	Glu	
						100					105					110	
	Gly	Ala	Gly	Glu	Leu	Val	Leu	Arg	Glu	Gly	Ala	Ala	Lys	Val	Ser	Trp	
						115					120					125	
40	Gln	Asp	His	His	Pro	Thr	Leu	Gln	Asp	Gln	Arg	Gln	Lys	Glu	Leu	Glu	
						130					135					140	

Ser Arg Gln Lys Met 1, Ser Trp Lys Thr Tyr Ile Glu Gly Trp Pro
 145 150 155 160
 Arg Cys Leu Asp His Glu Thr Val Lys Asp Leu Asp Leu Asn Ile Lys
 5 165 170 175
 Tyr Ser Ala Met Lys Asn Ala Lys Leu Phe Phe Lys Ala His Ser Ala
 180 185 190
 Tyr Thr Glu Leu Lys Val Lys Gly Leu Leu Asp Arg Thr Gly Leu Trp
 10 195 200 205
 Arg Ser Leu Arg Glu Met Arg Arg Leu Phe Asn Phe Arg Lys Thr Pro
 210 215 220
 Ala Ala Glu Tyr Val Phe Ala His Trp Gln Glu Asp Ala Phe Phe Ala
 15 225 230 235 240
 Ser Gln Phe Leu Asn Gly Ile Asn Pro Val Leu Ile Arg Arg Cys His
 245 250 255
 Ser Leu Pro Asn Asn Phe Pro Val Thr Asp Glu Met Val Ala Pro Val
 20 260 265 270
 Leu Gly Pro Gly Thr Ser Leu Gln Ala Glu Leu Glu Lys Gly Ser Leu
 275 280 285
 Phe Leu Val Asp His Gly Ile Leu Ser Gly Val His Thr Asn Ile Leu
 25 290 295 300
 Asn Gly Lys Pro Gln Phe Ser Ala Ala Pro Met Thr Leu Leu His Gln
 30 305 310 315 320
 Ser Ser Gly Ser Gly Pro Leu Leu Pro Ile Ala Ile Gln Leu Lys Gln
 325 330 335
 Thr Pro Gly Pro Asp Asn Pro Ile Phe Leu Pro Ser Asp Asp Thr Trp
 35 340 345 350
 Asp Trp Leu Leu Ala Lys Thr Trp Val Arg Asn Ser Glu Phe Tyr Ile
 355 360 365
 His Glu Ala Val Thr His Leu Leu His Ala His Leu Ile Pro Glu Val
 40 370 375 380

Phe Ala Leu Ala Thr Leu Arg Gln Leu Pro Arg Cys His Pro Leu Phe

385 390 395 400

5

Lys Leu Leu Ile Pro His Ile Arg Tyr Thr Leu His Ile Asn Thr Leu

405 410 415

Ala Arg Glu Leu Leu Val Ala Pro Gly Lys Leu Ile Asp Lys Ser Thr

420 425 430

10

Gly Leu Gly Thr Gly Gly Phe Ser Asp Leu Ile Lys Arg Asn Met Glu

435 440 445

Gln Leu Asn Tyr Ser Val Leu Cys Leu Pro Glu Asp Ile Arg Ala Arg

15

450 455 460

Gly Val Glu Asp Ile Pro Gly Tyr Tyr Tyr Arg Asp Asp Gly Met Gln

465 470 475 480

20

Ile Trp Gly Ala Ile Lys Ser Phe Val Ser Glu Ile Val Ser Ile Tyr

485 490 495

Tyr Pro Ser Asp Thr Ser Val Gln Asp Asp Gln Glu Leu Gln Ala Trp

500 505 510

25

Val Arg Glu Ile Phe Ser Glu Gly Phe Leu Gly Arg Glu Ser Ser Gly

515 520 525

Met Pro Ser Leu Leu Asp Thr Arg Glu Ala Leu Val Gln Tyr Ile Thr

30

530 535 540

Met Val Ile Phe Thr Cys Ser Ala Lys His Ala Ala Val Ser Ser Gly

545 550 555 560

35

Gln Phe Asp Ser Cys Val Trp Met Pro Asn Leu Pro Pro Thr Met Gln

565 570 575

Leu Pro Pro Pro Thr Ser Lys Gly Gln Ala Arg Pro Glu Ser Phe Ile

580 585 590

40

Ala Thr Leu Pro Ala Val Asn Ser Ser Ser Tyr His Ile Ile Ala Leu

595 600 605

Trp Leu Leu Ser Ala Glu Pro Gly Asp Gln Arg Pro Leu Gly His Tyr

610 615 620

Pro Asp Glu His Phe Thr Glu Asp Ala Pro Arg Arg Ser Val Ala Ala

625 630 635 640

5 Phe Gln Arg Lys Leu Ile Gln Ile Ser Lys Gly Ile Arg Glu Arg Asn

645 650 655

Arg Gly Leu Ala Leu Pro Tyr Thr Tyr Leu Asp Pro Pro Leu Ile Glu

10 660 665 670

Asn Ser Val Ser Ile

675

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

20 Trp Leu Leu Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- 30 (A) NAME/KEY: N=i=inosine
(B) LOCATION: 12, 15, 18
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACGTCTGGY TNYTNGCHAA A 21

35 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ix) FEATURE:
(A) NAME/KEY: N=i=inosine
(B) LOCATION: 12, 15, 18
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

10 xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACGTCTGGY TNYTNGCNAA G 21

(2) INFORMATION FOR SEQ ID NO:8:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

20 Gly Gln Leu Asp Trp
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCAAGTGAC CARTCNAGYT GNCC 24

30 (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAAGTGTAC CARTCRTAYT GNCC 24

(2) INFORMATION FOR SEQ ID NO:11:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (ix) FEATURE:

(A) NAME/KEY: N=i=inosine

(B) LOCATION: 24, 25

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAGTCGACTG GCTTYTGCC AAANNCTGGG TSCG 34

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGGATCCCT CCACCAGGNY TGSAGYTC 28

25 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGTATCTACT ACCCAAGTGA TGAG 24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TACCCAAGTG ATGAGTCTGT C 21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAAGACCTCA GGCAGCAGAT GTG 23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCATGGAAGG AGAACTCGGC AT 22

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACGGATCCAG CATGGCCGAG TTCAGGGTCA G 31

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

5 CGGAATTCAT GTCATCTGGG CCTGTGTTCC 30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGCCTCTCGC CATCCAGCT 19

(2) INFORMATION FOR SEQ ID NO:20:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTTCCCTG GGATTAGAT GGA 23

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGTATCTACT ACCCAAGTGA TGAG 24

30 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGGGATGTCA TCTGGGCCTG T 21

(2) INFORMATION FOR SEQ ID NO:23:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AACTCACCCC CACCACCATA CACA 24

(2) INFORMATION FOR SEQ ID NO:24:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTCCCGCCTC CATCTCCCA AGT 23

20 (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 662 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Gly Leu Tyr Arg Ile Arg Val Ser Thr Gly Ala Ser Leu Tyr Ala

1 5 10 15

30 Gly Ser Asn Asn Gln Val Gln Leu Trp Leu Val Gly Gln His Gly Glu

20 25 30

Ala Ala Leu Gly Lys Arg Leu Trp Pro Ala Arg Gly Lys Glu Thr Glu

35 40 45

35

	Leu Lys Val Glu Val Phe Glu Tyr Leu Gly Pro Leu Leu Phe Val Lys
	50 55 60
5	Leu Arg Lys Arg His Leu Leu Lys Asp Asp Ala Trp Phe Cys Asn Trp
	65 70 75 80
	Ile Ser Val Gln Gly Pro Gly Ala Gly Asp Glu Val Arg Phe Pro Cys
	85 90 95
10	Tyr Arg Trp Val Glu Gly Asn Gly Val Leu Ser Leu Pro Glu Gly Thr
	100 105 110
	Gly Arg Thr Val Gly Glu Asp Pro Gln Gly Leu Phe Gln Lys His Arg
	115 120 125
15	Glu Glu Glu Leu Glu Glu Arg Arg Lys Leu Tyr Arg Trp Gly Asn Trp
	130 135 140
20	Lys Asp Gly Leu Ile Leu Asn Met Ala Gly Ala Lys Leu Tyr Asp Leu
	145 150 155 160
	Pro Val Asp Glu Arg Phe Leu Glu Asp Lys Arg Val Asp Phe Glu Val
	165 170 175
25	Ser Leu Ala Lys Gly Leu Ala Asp Leu Ala Ile Lys Asp Ser Leu Asn
	180 185 190
	Val Leu Thr Cys Trp Lys Asp Leu Asp Asp Phe Asn Arg Ile Phe Trp
	195 200 205
30	Cys Gly Gln Ser Lys Leu Ala Glu Arg Val Arg Asp Ser Trp Lys Glu
	210 215 220
35	Asp Ala Leu Phe Gly Tyr Gln Phe Leu Asn Gly Ala Asn Pro Val Val
	225 230 235 240
	Leu Arg Arg Ser Ala His Leu Pro Ala Arg Leu Val Phe Pro Pro Gly
	245 250 255
40	Met Glu Glu Leu Gln Ala Gln Leu Glu Lys Glu Leu Glu Gly Gly Thr
	260 265 270
	Leu Phe Glu Ala Asp Phe Ser Leu Leu Asp Gly Ile Lys Ala Asn Val
	275 280 285

Ile Leu Cys Ser Gln Gln His Leu Ala Ala Pro Leu Val Met Leu Lys

290 295 300

Leu Gln Pro Asp Gly Lys Leu Leu Pro Met Val Ile Gln Leu Gln Leu

305 310 315 320

Pro Arg Thr Gly Ser Pro Pro Pro Pro Leu Phe Leu Pro Thr Asp Pro

325 330 335

Pro Met Ala Trp Leu Leu Ala Lys Cys Trp Val Arg Ser Ser Asp Phe

340 345 350

Gln Leu His Glu Leu Gln Ser His Leu Leu Arg Gly His Leu Met Ala

355 360 365

Glu Val Ile Val Val Ala Thr Met Arg Cys Leu Pro Ser Ile His Pro

370 375 380

Ile Phe Lys Leu Ile Ile Pro His Leu Arg Tyr Thr Leu Glu Ile Asn

385 390 395 400

Val Arg Ala Arg Thr Gly Leu Val Ser Asp Met Gly Ile Phe Asp Gln

405 410 415

Ile Met Ser Thr Gly Gly Gly Gly His Val Gln Leu Leu Lys Gln Ala

420 425 430

Gly Ala Phe Leu Thr Tyr Ser Ser Phe Cys Pro Pro Asp Asp Leu Ala

435 440 445

Asp Arg Gly Leu Leu Gly Val Lys Ser Ser Phe Tyr Ala Gln Asp Ala

450 455 460

Leu Arg Leu Trp Glu Ile Ile Tyr Arg Tyr Val Glu Gly Ile Val Ser

465 470 475 480

Leu His Tyr Lys Thr Asp Val Ala Val Lys Asp Asp Pro Glu Leu Gln

485 490 495

Thr Trp Cys Arg Glu Ile Thr Glu Ile Gly Leu Gln Gly Ala Gln Asp

500 505 510

Arg Gly Phe Pro Val Ser Leu Gln Ala Arg Asp Gln Val Cys His Phe

515 520 525

Val Thr Met Cys Ile Phe Thr Cys Thr Gly Gln His Ala Ser Val His

530 535 540

Leu Gly Gln Leu Asp Trp Tyr Ser Trp Val Pro Asn Ala Pro Cys Thr

5 545 550 555 560

Met Arg Leu Pro Pro Pro Thr Thr Lys Asp Ala Thr Leu Glu Thr Val

565 570 575

10 Met Ala Thr Leu Pro Asn Phe His Gln Ala Ser Leu Gln Met Ser Ile

580 585 590

Thr Trp Gln Leu Gly Arg Arg Gln Pro Val Met Val Ala Val Gly Gln

595 600 605

15 His Glu Glu Glu Tyr Phe Ser Gly Pro Glu Pro Lys Ala Val Leu Lys

610 615 620

Lys Phe Arg Glu Glu Leu Ala Ala Leu Asp Lys Glu Ile Glu Ile Arg

20 625 630 635 640

Asn Ala Lys Leu Asp Met Pro Tyr Glu Tyr Leu Arg Pro Ser Val Val

645 650 655

Glu Asn Ser Val Ala Ile

660

25 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Glu Leu Gln Xaa Trp Trp Tyr

1

5

(2) INFORMATION FOR SEQ ID NO:27:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Asp Val Trp Leu Leu Ala Lys
1 5

5 (2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gly Gln Phe Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:29:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCAAGCGCAS SARTCRAAYT GNCC 24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAGCTTTGTC TCTGAAATAG TCAG 24

30 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTGAGGAATC AATAGCTTGA AGAG 24

(2) INFORMATION FOR SEQ ID NO:32:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GATGTGTGAC AGCCTCATGG ATG 23

(2) INFORMATION FOR SEQ ID NO:33:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAGCTTAGG AGGATGGCGA AATGCAGG 28

20 (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGAATTCATG TTAGATGGAG ACACTGTT 28

(2) INFORMATION FOR SEQ ID NO:35:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Gln Tyr Asp Trp
1 5

(2) INFORMATION FOR SEQ ID NO:36:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Xaa Val Asp Trp Leu Leu Ala Ala Lys Xaa Trp Val Arg
1 5 10

It will be understood that various details of the invention may be
changed without departing from the scope of the invention. Furthermore,
15 the foregoing description is for the purpose of illustration only, and not for
the purpose of limitation--the invention being defined by the claims.